Genomics reference resource for African cattle

An initiative of the dairy genomics program of the Centre for Tropical Livestock Genetics and Health

Centre for Tropical Livestock Genetics and Health

The Centre for Tropical Livestock Genetics and Health supports programs that improve livestock-based livelihoods in the tropics. It is a strategic alliance of the International Livestock Research Institute, the Roslin Institute at the University of Edinburgh, and Scotland's Rural College. ctlgh.org

The dairy genomics program

The dairy genomics program seeks to facilitate the application of genomics to dairy production in the tropics for increased livestock productivity, enhanced livelihoods of the rural poor, increased food and nutritional security, and more sustainable environmental development.

This will be achieved through the:

- Identification of, and advocacy for, key applications of genomics to dairy production in the tropics
- Support for the development of tools and methodological approaches to facilitate the above identified applications
- Delivery of capacity building training
- Establishment of research and resource mobilisation partnerships

Description

A collated set of sequence and genotype information on cattle breeds in Africa is currently not available. Such a resource is important as it can underpin the design of genomic tools for different applications.

In collaboration with African partners, the dairy genomics program will facilitate the generation of this important resource by collating data already available in public databases and data with private research groups (where access is granted) and through the generation of new data.

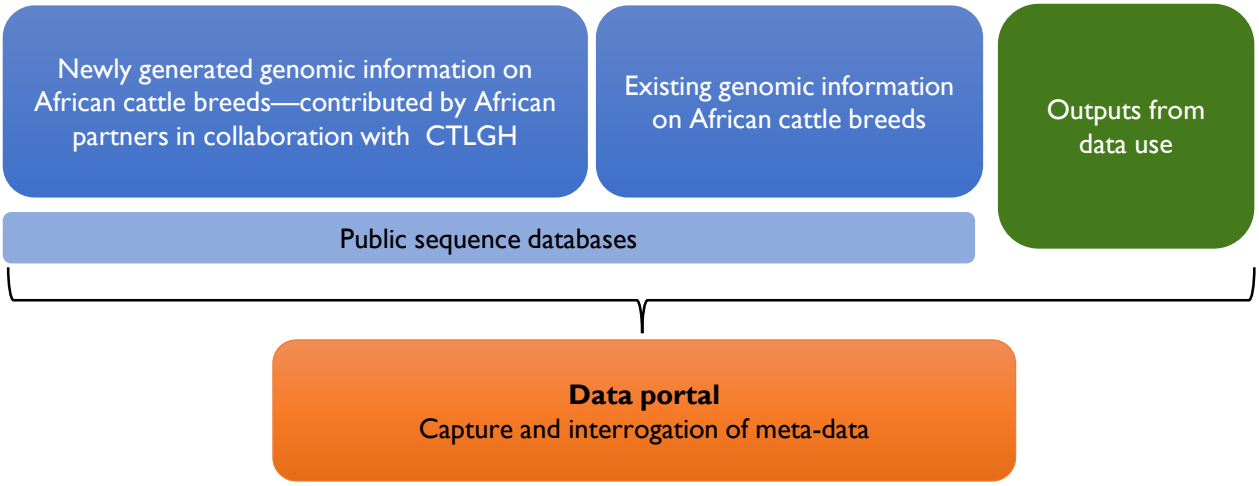
A schema of the genomic reference resource is given below. It will comprise the genomic data on African cattle breeds, meta-data on the sequenced or genotyped animals (such as their GPS location at time of sampling), as well as well documented and easily searchable outputs arising from the use of the data (tools, publications, etc.). The entry point to this will be a website and data-portal, which captures meta-data and allows for it to be easily searched, browsed, analysed and used. The raw genomic data will be archived in the major public sequence databases (NCBI www.ncbi.nlm.nih.gov and EMBL-EBI www.ebi.ac.uk).

The initial target for the resource is 25 African cattle breeds with sequence information on at least 10 individual animals per breed by the end of 2017. The expectation is that the number of breeds, and individual animals per breed, will increase over time, as the initiative gains momentum and additional resources become available.

Intended use

It is intended that the resource be used by the African and international research community in cattle genomics for the ultimate benefit of African livestock keepers, other livestock value chain actors and animal-source food consumers. To this end the dairy genomics program will also facilitate the capacity building of African researchers in the field of genomics.

Schema for the genomics reference resource for African cattle



In the first instance, this CLTGH program intends to use the resource to:

- Identify sets of informative single-nucleotide polymorphisms (SNPs) that can inform the design of SNP-chips customized for African cattle populations and particular applications. Such applications include genomic analysis aimed at identifying genes or gene networks underpinning important livestock adaptation or production traits—potentially leading to the creation of new or improved breed-types, or within breed-improvement programs to determine the relatedness amongst individual animals in the absence of pedigree and/or to predict breeding values.
- Develop a smart-tool to determine the breed composition of African cattle based on SNP-genotyping. Such a tool can be used in studies comparing the performance of, or household income from keeping, different breeds or crossbreeds, and thus the identification of the most appropriate breed-type(s) for particular production systems and environments (for example, Marshall et al. 2016)

Contributors

All contributors to the resource will be fully acknowledged, with a list maintained on the data portal. Genomic information submitted to public sequence databases will be jointly attributed to the African partner involved in generating that sequence information and CTLGH.

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CGIAR RESEARCH PROGRAM ON Livestock and Fish

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